Retrieve Application SCORE System

# SCORE Search Results Details for Application 09961086 and Search Result 20080917 142911 us-09-961-086a-1.rpr.

Page	Overview	FAQ			

This page gives you Search Results detail for the Application 09961086 and Search Result 20080917 142911 us-09-961-086a-1.

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OM protein - protein search, using sw model

Run on: September 18, 2008, 22:00:18 : Search time 41 Seconds

(without alignments)

1537.121 Million cell updates/sec

SCORE Comments /

Title. IIS-09-961-086A-1

Perfect score: 3352

1 MSSSNVEVFIPVSOGNTNGF.....MIVIFLTIAYLKLLFLKKYS 655 Sequence:

Scoring table: BLOSUM62

Score Home

Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

PIR 80:\* 1: pir1:\*

Database :

2: pir2:\* 3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARTES

		8				
Result No.	Score	Query Match	Length	DB	ID	Description
1	2849.5	85.0	656	2	JC7860	brain multidrug re
2	835.5	24.9	1049	1	S19421	ATP-dependent perm

2	010	0.4.0	607	-	marmer.	1.11
3 4	812 800.5	24.2	687 737	1	FYFFW	white protein - fr
5	774	23.9	646	2	T46101	ABC transporter-li
6	767.5	23.1		2	C86441	probable ABC trans
	746		687		D96553	hypothetical prote
7		22.3	649	2	A84509	probable ABC trans
8	745	22.2	725	2	T47652	ABC transporter-li
9	741.5	22.1	739	2	T45891	ABC transporter-li
10	739	22.0	678	2	H96552	hypothetical prote
11	726.5	21.7	708	2	T47650	ABC transporter-li
12	721	21.5	635	2	T08934	hypothetical prote
13	720.5	21.5	755	2	G84791	probable ABC trans
14	717.5	21.4	740	1	T02567	probable ATP-bindi
15	712.5	21.3	609	2	E96742	probable ABC trans
16	710	21.2	638	2	G02068	white homolog - hu
17	708	21.1	646	2	JC7777	ATP binding casset
18	707.5	21.1	547	2	T31543	hypothetical prote
19	707.5	21.1	720	2	T47648	ABC transporter-li
20	677	20.2	559	2	B88474	protein C05D10.3 [
21	676	20.2	725	2	C84423	probable ABC trans
22	669	20.0	659	2	E86313	hypothetical prote
23	664	19.8	608	2	T34391	hypothetical prote
24	660	19.7	662	2	T47649	ABC transporter-li
25	658.5	19.6	1294	2	S77690	probable membrane
26	657.5	19.6	1450	2	T45888	ABC transporter-li
27	656.5	19.6	590	2	B96573	protein F12M16.17
28	649.5	19.4	633	2	T19189	hypothetical prote
29	645.5	19.3	577	2	T04229	ABC-type transport
30	639	19.1	658	2	T31958	hypothetical prote
31	636.5	19.0	639	2	G88839	protein C10C6.5 [i
32	636.5	19.0	695	2	T21109	hypothetical prote
33	627.5	18.7	610	2	T19333	hypothetical prote
34	612.5	18.3	1501	2	S50992	SNQ2 protein - yea
35	612	18.3	1530	2	S52239	brefeldin a resist
36	603	18.0	1530	2	T52010	hypothetical prote
37	602	18.0	1511	2	A53151	pleiotropic drug r
38	594	17.7	1564	2	S55517	probable transport
39	593	17.7	1443	2	T02491	probable ABC trans
40	590	17.6	1469	2	H96622	probable ABC trans
41	585	17.5	1333	2	S63403	probable membrane
42	580.5	17.3	1420	2	T02644	ABC-type transport
43	580.5	17.3	1529	2	S69688	hypothetical prote
44	572	17.1	1413	2	G84790	probable ABC trans
45	564	16.8	1466	2	T30566	ATP-binding casset

#### ALIGNMENTS

```
RESULT 1
JC7860
```

brain multidrug resistance protein, BMDP - pig

C; Species: Sus scrofa domestica (domestic pig)

C;Date: 18-Nov-2002 #sequence\_revision 18-Nov-2002 #text\_change 09-Jul-2004 C;Accession: JC7860

R; Eisenblaetter, T.; Galla, H.J.

Biochem. Biophys. Res. Commun. 293, 1273-1278, 2002

A:Title: A new multidrug resistance protein at the blood-brain barrier.

SCORE Search Results Details for Application 09961086 and Search Result 20080917\_142911\_us-09-961-086a-1.rpr. A; Reference number: JC7860; MUID: 22050127; PMID: 12054514 A:Accession: JC7860 A; Molecule type: mRNA A:Residues: 1-656 <EIS> A;Cross-references: UNIPROT:Q8MIB3; UNIPARC:UPI0000087EC5; GB:AJ420927 A:Experimental source: brain C; Comment: This protein, a new transport protein of the ATP-binding cassette (ABC) superfamily of transporters, expressed in porcine brain capillary endothelial cells, plays an importnat role in the exclusion of xenobiotics from the brain and participates in drug transport across the blood-brain barrier and therefore is considered as a efflux pump at the cerebral endothelium. C:Genetics: A; Gene: bmdp Query Match 85.0%; Score 2849.5; DB 2; Length 656; Best Local Similarity 84.3%; Pred. No. 2.7e-192; Matches 553; Conservative 44; Mismatches 58; Indels 1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60 Qv Db 1 MSSNSYOVSIPMSKRNTNGLPGSSSNELKTSAGGAVLSFHDICYRVKVKSGFLFCRKTVE 60 61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120 Qv 61 KEILTNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPHGLSGDVLINGAPRPANFKCN 120 Db Qv 121 SGYVVODDVVMGTLTVRENLOFSAALRLATTMTNHEKNERINRVIOELGLDKVADSKVGT 180 121 SGYVVODDVVMGTLTVRENLOFSAALRLPTTMTNHEKNERINMVIOELGLDKVADSKVGT 180 181 OFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLKRMSKOGRTIIF 240 181 OFIRGVSGGERKRTSIAMELITDPSILFLDEPTTGLDSSTANAVLLLKRMSKOGRTIIF 240 241 SIHOPRYSIFKLFDSLTLLASGRLMFHGPAOEALGYFESAGYHCEAYNNPADFFLDIING 300 Qv 241 SIHOPRYSIFKLFDSLTLLASGRLMFHGPAREALGYFASIGYNCEPYNNPADFFLDVING 300 Πh 301 DSTAVALNR-EEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHOLSGGEKKK 359 301 DSSAVVLSRADRDEGAOEPEEPPEKDTPLIDKLAAFYTNSSFFKDTKVELDOFSGGRKKK 360 Db 360 KITVFKEISYTTSFCHOLRWVSKRSFKNLLGNPOASIAOIIVTVVLGLVIGAIYFGLKND 419 361 KSSVYKEVTYTTSFCHOLRWISRRSFKNLLGNPOASVAOIIVTIILGLVIGAIFYDLKND 420 Db

481 PMRMLPSIIFTCITYFLLGLKPAVGSFFIMMFTLMMVAYSASSMALAIAAGQSVVSVATL 540
540 LMTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATG 599

541 LMTISFVFMMIFSGLLVNLKTVVPWLSWLOYFSIPRYGFSALOYNEFLGONFCPGLNVTT 600

0v

Πh

Db

```
600 NNPCNYATCTGEEYLVKOGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
Qу
Πh
          601 NNTCSFAICTGAEYLENOGISLSAWGLWONHVALACMMVIFLTIAYLKLLLKKYS 656
RESULT 2
$19421
ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YCR011c; protein YCR105
C; Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C; Accession: S19421; S40914
R; Goffeau, A.; Purnelle, B.; Skala, J.
submitted to the Protein Sequence Database, March 1992
A; Reference number: S19420
A; Accession: S19421
A; Molecule type: DNA
A; Residues: 1-1049 <GOF>
A; Cross-references: UNIPROT: P25371; UNIPARC: UPI00001255FD; EMBL: X59720; NID: q1907116; PIDN:
CAA42328.1; PID:q1907154; GSPDB:GN00003; MIPS:YCR011c
R; Purnelle, B.; Skala, J.; Goffeau, A.
Yeast 7, 867-872, 1991
A; Title: The product of the YCR105 gene located on the chromosome III from Saccharomyces
cerevisiae presents homologies to ATP-dependent permeases.
A; Reference number: S40914; MUID: 92160395; PMID: 1789009
A:Accession: S40914
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-1049 < PUR>
A; Cross-references: UNIPARC: UPI00001255FD
R; Skala, J.; Purnelle, B.; Goffeau, A.
Yeast 8, 409-417, 1992
A:Title: The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of
chromosome III from Saccharomyces cerevisiae reveals seven open reading frames including
the RVS161, ADP1 and PGK genes.
A; Reference number: S25353; MUID: 92327849; PMID: 1626432
A; Contents: annotation
C:Genetics:
A; Gene: SGD: ADP1; MIPS: YCR011c
A; Cross-references: SGD:S0000604; MIPS:YCR011c
A; Map position: 3R
C; Superfamily: ATP-dependent permease ADP1; ATP-binding cassette homology
C; Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F;26-1049/Product: ATP-dependent permease ADP1 #status predicted <MAT>
F;26-324/Domain: extracellular #status predicted <EXT>
F;325-341/Domain: transmembrane #status predicted <TM1>
F;406-607/Domain: ATP-binding cassette homology <ABC>
F;423-430/Region: nucleotide-binding motif A (P-loop)
F:550-557/Region: nucleotide-binding motif B
F;794-810/Domain: transmembrane #status predicted <TM2>
F;829-845/Domain: transmembrane #status predicted <TM3>
F;878-894/Domain: transmembrane #status predicted <TM4>
F:909-925/Domain: transmembrane #status predicted <TM5>
```

F;938-954/Domain: transmembrane #status predicted <TM6>
F;1025-1041/Domain: transmembrane #status predicted <TM7>

F;50,114,165,221/Binding site: carbohydrate (Asn) (covalent) #status predicted F;429/Binding site: ATP (Lys) #status predicted

```
Query Match 24.9%; Score 835.5; DB 1; Length 1049;
  Best Local Similarity 30.5%; Pred. No. 1.8e-50;
  Matches 222; Conservative 134; Mismatches 257; Indels 115; Gaps 18;
                 1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
                     Db
              355 LGSSKSPIRLP-DEDAVNNFLONEDDTL----ATLSFENITYSVPSINS----DGVE 402
               61 KEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRP-ANFK 118
Qу
                     403 ETVLNEISGIVKPGQILAIMGGSGAGKTTLLDILAMKRKTGHVSGSIKVNGISMDRKSFS 462
Dh
               119 CNSGYVVODDVVMGTLTVRENLOFSAALRLATTMTNHEKNERINRVIOELGLDKVADSKV 178
Οv
                          1:| | | | | :: | | | | | | : | | | | | :: | | | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
               463 KIIGFVDODDFLLPTLTVFETVLNSALLRLPKALSFEAKKARVYKVLEELRIIDIKDRII 522
Dh
Qу
               179 GTOFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLKRMSKO-GRT 237
                    523 GNEFDRGISGGEKRRVSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVRLSSDYNRT 582
              238 IIFSIHOPRYSIFKLFDSLTLLASGRLMFHGPAOEALGYFESAGYHCEAYNNPADFFLDI 297
                     583 LVLSIHOPRSNIFYLFDKLVLLSKGEMVYSGNAKKVSEFLRNEGYICPDNYNIADYLIDI 642
Dh
              298 -----INGDSTAV 305
                                                                                                      : |
              643 TFEAGPOGKRRRIRNISDLEAGTDTNDIDNTIHOTTFTSSDGTTOREWAHLAAHRDEIRS 702
               306 ALNREEDFKATE----IIEPSKODKPLIEKLAEIYVNSSFYKETKAELHO-LSGGEKKKK 360
Οv
                      703 LLRDEEDVEGTDGRRGATEIDLNTKLLHDK----YKDSVYYAELSOEIEEVLSEGDEESN 758
               361 IT--VFKEISYTTSFCHOLRWVSKRSFKNLLGNPOASIAOIIVTVVLGLVIGAIYFGLKN 418
0v
                    759 VLNGDLPTGOOSAGFLOOLSILNSRSFKNMYRNPKLLLGNYLLTILLSLFLGTLYYNVSN 818
               419 DSTGIONRAGVLFFLTTNOCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDL 478
                    819 DISGFONRMGLFFFILTYFGFVTFTGLSSFALERIIFIKERSNNYYSPLAYYISKIMSEV 878
Dh
              479 LPMTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVAT 538
                     879 VPLRVVPPILLSLIVYPMTGLNMKDNAFFKCIGILILFNLGISLEILTIGIIFEDLNNSI 938
Db
               539 LLMTICFVFMMIFSGLLV---NLTTIASWLSWLQYFSIPRYGFTALQHNEF----- 586
                     :| : : ::|||| : |:| :| :|: ||: ||: ||
               939 ILSVLVLLGSLLFSGLFINTKNITNVA--FKYLKNFSVFYYAYESLLINEVKTLMLKERK 996
               587 LGQNF-CPGLNATGNNPCNYATCTGEEYLVKQGI--DLSPWGLWKNHVALACMIVIFLTI 643
                     997 YGLNIEVPG-----ATILSTFGFVVQNLVFDIK-----ILALFNVVFLIM 1036
               644 AYLKLLFL 651
                      11 1 ::
```

```
Db 1037 GYLALKWI 1044
```

Db

Οv

```
RESULT 3
FYFFW
white protein - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C;Date: 31-Dec-1990 #sequence_revision 17-Feb-1995 #text_change 09-Jul-2004
C; Accession: S08635; S07263; S10240
R: Pepling, M.: Mount, S.M.
Nucleic Acids Res. 18, 1633, 1990
A; Title: Sequence of a cDNA from the Drosophila melanogaster white gene.
A; Reference number: S08635; MUID: 90221897; PMID: 2109311
A:Accession: S08635
A; Molecule type: mRNA
A:Residues: 1-687 <PEP>
A; Cross-references: UNIPROT: P10090; UNIPARC: UPI000011F0A1; EMBL: X51749; NID: q8825; PIDN:
CAA36038.1; PID: q8826
R;O'Hare, K.; Murphy, C.; Levis, R.; Rubin, G.M.
J. Mol. Biol. 180, 437-455, 1984
A; Title: DNA sequence of the white locus of Drosophila melanogaster.
A; Reference number: S07263; MUID: 85134865; PMID: 6084717
A; Accession: S07263
A; Molecule type: DNA
A; Residues: 1-24, 'LIFEIPYHCRVTAD', 30-
334, 'ITLHLNSYPAWVPSVLPTTIRRTFTYRCWPLCPDGRSSPVIGSPRYG', 372-687 < OHA1>
A:Cross-references: UNIPARC:UPI000016B571; EMBL:X02974
A; Experimental source: strain Canton S
R:O'Hare, K.
submitted to the EMBL Data Library, June 1985
A; Reference number: S10240
A; Accession: S10240
A; Molecule type: DNA
A; Residues: 1-24, 'LIFEIPYHCRVTAD', 30-687 < OHA2>
A; Cross-references: UNIPARC: UPI000016BDFF; EMBL: X02974; NID: g10873; PIDN: CAA26716.1; PID:
q10874
A; Experimental source: strain Canton S
C; Genetics:
A:Gene: white: w
A; Cross-references: FlyBase: FBgn0003996
A; Introns: 24/3; 116/1; 334/2; 439/3; 483/3
C; Superfamily: fruit fly white protein; ATP-binding cassette homology
C; Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F;113-317/Domain: ATP-binding cassette homology <ABC>
F:130-137/Region: nucleotide-binding motif A (P-loop)
F;261-265/Region: nucleotide-binding motif B
F;67,93,472,554,651/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Ouerv Match
                          24.2%: Score 812: DB 1: Length 687:
 Best Local Similarity 32.1%; Pred. No. 4.4e-49;
 Matches 210: Conservative 134: Mismatches 251: Indels 60: Gaps
           5 NVEVFIPVSOGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVEKEIL 64
                             1 :
                                    | | | | : :|
                                                               1 :
```

74 NMDIFGAVNO-----PGSGWROLVNRTRGLFCNERHI-----PAPR---KHLL 113

65 SNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGL----SGDVLINGAPRPA-NFK 118

Dh

```
119 CNSGYVVODDVVMGTLTVRENLOFSAALRLATTMTNHEKNERINRVIOELGLDKVADSKV 178
              173 ARCAYVOODDLFIGSLTAREHLIFOAMVRMPRHLTYRORVARVDOVIOELSLSKCOHTII 232
Db
        179 GTO-FIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKOGRT 237
               ::|:|||||||
        233 GVPGRVKGLSGGERKRLAFASEALTDPPLLICDEPTSGLDSFTAHSVVOVLKKLSOKGKT 292
        238 IIFSIHOPRYSIFKLFDSLTLLASGRLMFHGPAOEALGYFESAGYHCEAYNNPADFFLDI 297
Qу
           293 VILTIHOPSSELFELFDKILLMAEGRVAFLGTPSEAVDFFSYVGAOCPTNYNPADFYVOV 352
Dh
        298 INGDSTAVALNREEDFKATEIIEPSKODKPLIEKLAEIYVNSSFYKETKAELHOLSGGEK 357
               11 11 : :
                                    353 L----AVVPGREIESR------DRIAKICDNFAISKVAR-DMEOLLATKN 391
Db
        358 KKKITVFKEISYT--TSFCHOLRWVSKRSFKNLLGNPOASIAOIIVTVVLGLVIGAIYFG 415
               392 LEKPLEOPENGYTYKATWFMOFRAVLWRSWLSVLKEPLLVKVRLIOTTMVAILIGLIFLG 451
        416 LKNDSTGIONRAGVLFFLTTNOCFSSVSA-VELFVVEKKLFIHEYISGYYRVSSYFLGKL 474
               452 OOLTOVGVMNINGAIFLFLTNMTFONVFATINVFTSELPVFMREARSRLYRCDTYFLGKT 511
Dh
        475 LSDLLPMTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGOSVV 534
0v
           Dh
        512 IAE-LPLFLTVPLVFTAIAYPMIGLRAGVLHFFNCLALVTLVANVSTSFGYLISCASSST 570
        535 SVATLLMTICFVFMMIFSGLLVNLTTIASWLSWLOYFSIPRYGFTALOHNEFLGONFCPG 594
           571 SMALSVGPPVIIPFLLFGGFFLNSGSVPVYLKWLSYLSWFRYANEGLLINQWADVE--PG 628
Db
        595 -LNATGNNPCNYATCTGEEYLVKOGIDLSPWGLWKNHVALACMIVIFLTIAYLKL 648
0v
            :: | : | | | | | | :: : : | | | :: | | | :| | | |
        629 EISCTSSN----TTCPSSGKVILETLNFSAADLPLDYVGLAILIVSFRVLAYLAL 679
Db
RESULT 4
T46101
ABC transporter-like protein - Arabidopsis thaliana
N; Alternate names: protein T25B15.80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46101
R; Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
```

A;Cross-references: UNIPROT:Q9FT51; UNIPARC:UPI00000A69DB; EMBL:AL132972

A; Experimental source: cultivar Columbia; BAC clone T25B15

A;Reference number: Z23021 A;Accession: T46101 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-737 <ALC>

```
C; Genetics:
A; Map position: 3
A;Introns: 122/1; 146/3; 225/2; 277/2; 338/3; 422/2; 535/1; 628/3; 664/3
A:Note: T25B15.80
 Query Match
                 23.9%; Score 800.5; DB 2; Length 737;
 Best Local Similarity 31.4%; Pred. No. 3.1e-48;
 Matches 211; Conservative 132; Mismatches 227; Indels 101; Gaps 21;
      27 DLKAFTEGAV-----LSFHNICYRVKLKSGFLPCRKPVEKEILSNINGIMKPG- 74
         124 DIEAATSSVVKFOAEPTFPIYLKFIDITYKVTTKG----MTSSSEKSILNGISGSAYPGE 179
Db
       75 LNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCNSGYVVODDVVMGTL 134
          180 LLALMGPSGSGKTTLLNALGGRFNOONIGGSVSYNDKPYSKHLKTRIGFVTODDVLFPHL 239
      135 TVRENLOFSAALRLATTMTNHEKNERINRVIOELGLDKVADSKVGTOFIRGVSGGERKRT 194
          Dh
      240 TVKETLTYTALLRLPKTLTEOEKEORAASVIOELGLERCODTMIGGSFVRGVSGGERKRV 299
      195 SIGMELITDPSILFLDEPTTGLDSSTANAVLLLKRMSKOGRTIIFSIHOPRYSIFKLFD 254
Οv
          300 CIGNEIMTNPSLLLLDEPTSSLDSTTALKIVOMLHCIAKAGKTIVTTIHOPSSRLFHRFD 359
Db
      255 SLTLLASGRLMFHGPAOEALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNREEDFK 314
QУ
          360 KLVVLSRGSLLYFGKASEAMSYFSSIGCSPLLAMNPAEFLLDLVNGNMNDIS----- 411
      315 ATEIIEPSKODKPLIEKLAEIYVNS-----SFYKETKAELHOLS-----GGE 356
            412 ----VPSALKEKMKIIRL-ELYVRNVKCDVETOYLEEAYKTOIAVMEKMKLMAPVPLDEE 466
Db
      357 KKKKITVFKE---ISYTTSFC-HOLRWVSKRS---FKNLLGNPOASIAOIIVTVVLGLVI 409
0v
          467 VKLMITCPKREWGLSWWEOYCLLSLRGIKERRHDYFSWL-----RVTOVLSTAI---IL 517
Dh
       410 GAIYFGLKNDSTGIO-NRAGVLFFLTTNOCFSSV-SAVELFVVEKKLFIHEYISGYYRVS 467
         Db
       518 GLLWW--OSDITSORPTRSGLLFFIAVFWGFFPVFTAIFTFPOERAMLSKERESNMYRLS 575
      468 SYFLGKLISDLIPMTMLPSTTFTCTVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAT 527
          576 AYFVARTTSD-LPLDLILPVLFLVVVYFMAGLRLRAESFFLSVLTVFLCIVAAQGLGLAI 634
Db
      528 AAGOSVVSVATLLMTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTAL---QHN 584
Qv
          635 GASLMDLKKATTLASVTVMTFMLAGGYFVK--KVPFFIAWIRFMSFNYHTYKLLVKVQYE 692
Dh
Qу
      585 EFLGONFCPGLNATGNNPCNYATCTGEEYLVKOGIDLSPWGLWKNHVALACMIVIFLTIA 644
                693 EIM-----ESVNGEE-IESGL----KEVSALVAMIIGYRLVA 724
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645 YLKLLFLKKYS 655

1 1 :1 :1

725 YFSLRRMKLHS 735

Qv

Db

RESHLT 5

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C86441
probable ABC transporter [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: C86441
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.;
Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.;
Creasy, T.H.; Dewar, K.; Dunn, P.; Etqu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.
Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.;
Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.;
Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti,
R.; Marziali, A.; Militscher, J.; Miranda, M.; Nquyen, M.; Nierman, W.C.; Osborne, B.I.;
Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.
J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.;
Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
A:Accession: C86441
A; Status: preliminary
A; Molecule type: DNA
A:Residues: 1-646 <STO>
A; Cross-references: UNIPROT: 09C6R7; UNIPARC: UPI00000AA9CB; GB: AE005172; NID: g11136734; PIDN:
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C; Genetics:
A; Map position: 1
C; Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-
binding cassette homology
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   Best Local Similarity 33.5%; Pred. No. 1.9e-46;
   Matches 213; Conservative 119; Mismatches 234; Indels 70; Gaps
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Qy
                           51 ITLKEVVYKVKIEOTSOCMGSWKSKEKTILNGITGMVCPGEFLAMLGPSGSGKTTLLSAL 110
Db
                 94 AARKDPSGLSGDVLINGAPRPANFKCNSGYVVODDVVMGTLTVRENLOFSAALRLATTMT 153
                          111 GGRLSKT-FSGKVMYNGOPFSGCIKRRTGFVAODDVLYPHLTVWETLFFTALLRLPSSLT 169
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               154 NHEKNERINRVIQELGLDKVADSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLDEPT 213
                          170 RDEKAEHVDRVIAELGLNRCTNSMIGGPLFRGISGGEKKRVSIGOEMLINPSLLLLDEPT 229
               214 TGLDSSTANAVLLLKRMSKOGRTIIFSIHOPRYSIFKLFDSLTLLASGRLMFHGPAOEA 273
                       :||||:||: :: :||:: |||:: :||| | ||: :|| : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
Dh
               230 SGLDSTTAHRIVTTIKRLASGGRTVVTTIHQPSSRIYHMFDKVVLLSEGSPIYYGAASSA 289
               274 LGYFESAGYHCEAYNNPADFFLDIING--DSTAVALNREEDFKATEIIEPSKODKPLIEK 331
                                             : : : |
                                                                                           1: | :| : |
Db
               290 VEYFSSLGFSTSLTVNPADLLLDLANGIPPDTOKETSEOEOKTVKETL-VSAYEKNISTK 348
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332 L-AEI-YVNSSFYKETKAELHOLSGGEKKKKITVFKEISYTTSFCHOL----RWVSKRS 384
                  | |: ||| | : |:: :|
        349 LKAELCNAESHSYEYTKAAAKNL-----KSEOWCTTWWYOFTVLLORGVRERR 396
Πh
        385 FKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFLTTNQCFSSV-S 443
QУ
                 Πh
        397 FESF---NKLRIFOVISVAFLG---GLLWW--HTPKSHIODRTALLFFFSVFWGFYPLYN 448
        444 AVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLPMTMLPSIIFTCIVYFMLGLKPKA 503
            449 AVFTFPOEKRMLIKERSSGMYRLSSYFMARNVGD-LPLELALPTAFVFIIYWMGGLKPDP 507
Db
        504 DAFFVMMFTLMMVAYS---ASSMALAIAAGOSVVSVATLLMTICFVFMMIFSGLLVNLTT 560
             508 TTF---ILSLLVVLYSVLVAOGLGLAFGALLMNIKOATTLASVTTLVFLIAGGYYVO--O 562
Db
        561 IASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGNNPCNYATCT-----GEEY 613
           Dh
        563 IPPFIVWLKYLSYSYYCYKLLL-----GIOYTDD---DYYECSKGVWCRVGDFP 608
        614 LVK-OGIDLSPWGLWKNHVALACMIVIFLTIAYLKL 648
Οv
            :| |:: || : |:| : |:| : |
Dh
        609 AIKSMGLN----NLWIDVFVMGVMLVGYRLMAYMAL 640
RESULT 6
D96553
hypothetical protein F5D21.6 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D96553
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.;
Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.;
Creasy, T.H.; Dewar, K.; Dunn, P.; Etqu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.
Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
```

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L. J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID: 21016719; PMID: 11130712

A:Accession: D96553

A; Status: preliminary A:Molecule type: DNA

A; Residues: 1-687 <STO>

A; Cross-references: UNIPROT:Q9C8K2; UNIPARC:UPI000000AB8E7; GB:AE005173; NID:g10092349; PIDN: AAG12758.1; GSPDB:GN00141

C: Genetics:

A; Gene: F5D21.6 A: Map position: 1 C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-binding cassette homology

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                 22.9%; Score 767.5; DB 2; Length 687;
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       34 GAVLSFHNICYRVKLKSGFLPCRKPVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDV 92
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       93 LAARKDPSG-LSGDVLINGAPRPANFKCNSGYVVODDVVMGTLTVRENLOFSAALRLATT 151
Qу
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Dh
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Dh
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      271 OEALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNREEDFKATEIIEPSKODKPLIE 330
          254 KFAVEFFAEAGFPCPKKRNPSDHFLRCINSDFDTVTATLKGSORIRE--TPATSD-PLMN 310
Dh
       331 -----KLAEIYVNSSFYKETKAELHQLSGGE-----KKKKITVFKEISYTTSFC 374
0v
                311 LATSEIKARLVENYRRSVYAKSAKSRIRELASIEGHHGMEVRKGSEATWFK----- 361
       375 HOLRWYSKRSFKNLLGNPOASIAOIIVTVVLGLVIGAIYFGLKNDSTGIONRAGVLFFLT 434
Οv
          362 -OLRTLTKRSFVNMCRDIGYYWSRIVIYIVVSFCVGTIFYDVGHSYTSILARVSCGGFIT 420
       435 TNOCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLPMTMLPSIIFTCIVY 494
0v
             421 GFMTFMSIGGFPSFIEEMKVFYKERLSGYYGVSVYIISNYVSS-FPFLVAIALITGSITY 479
       495 FMLGLKPKAD--AFF-----VMMFTLMMVAYSASSMALAIAAGQSVVSVATLLMTI 543
          1: :1 111
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Dh
      544 CFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQ---HNEFLGONFCPGLNATGN 600
                538 GFF-----RLLPDLPKV----FWRYPISFMSYGSWAIQGAYKNDFLGLEFDPMF---- 582
      601 NPCNYATCTGEEYLVK-QGIDLSP---WGLWKNHVALACMIVIFLTIAYLK 647
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RESULT 7 A84509

probable ABC transporter [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #text change 09-Jul-2004

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C;Accession: A84509
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R,Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H. M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197

A; Accession: A84509

A; Status: preliminary A; Molecule type: DNA

A; Residues: 1-649 <STO>

A;Cross-references: UNIPROT:Q9SIT6; UNIPARC:UPI00000A95A1; GB:AE002093; NID:g4558665; PIDN: AAD22683.1; GSPDB:GN00139

C; Genetics:

A; Gene: At2g13610

A; Map position: 2

 $\hbox{C;Superfamily: Arabidops is thaliana probable ATP-binding cassette protein F12L6.1; ATP-binding cassette homology}$ 

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Db	:  :    :   :  :     ::       :          0 KHVLKGVTCRAKPWEILAIVGPSGAGKSSLLEILAARLIPQTGSVYVNKRPVDRANFK 117
Qy	9 CNSGYVVQDDVVMGTLTVRENLQFSAALRLATTMINHEKNERINRVIQELGLDKVADSKV 178
Db	8 KISGYVTQKDTLFPLLTVEETLLFSAKLRLKLPADELRSRVKSLVHELGLEAVATARV 175
Qy	9 GTQFIRGVSGGERKRTSIGMELITDPSLIFLDEPTTGLDSSTANAVLLLLKRMSK-QGRT 237
Db	6 GDDSVRGISGGERRRVSIGVEVIHDPKVLILDEPTSGLDSTSALLIIDMLKHMAETRGRT 235
Qy	8 IIFSIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDI 297
Db	6 IILTIHQPGFRIVKQFNSVLLLANGSTLKQGSVDQLGVYLRSNGLHPPLHENIVEFAIES 295
Qy	8 INGDSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEK 357
Db	6 I-ESITKQQRLQESRRAAHVLTPQTTLQEKRSEDSQGESKSGKFTLQQLFQQTR 348
Qy	8 KKKI-TVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAI 412 :  :         : : :
Db	9 VADVGTMNIATEFTRDFANSRLEETMILTHRFSKNIFRTKELFACRTVQMLGSGIVLGLI 408
Qy	3 YFGLKNDSTGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLG 472
Db	9 FHNLKDDLKGARERVGLFAFILTFLLTSTIEALPIFLQEREILMKETSSGSYRVSSYAVA 468
Qy	3 KLLSDLLPMTMLPSIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAA 529
Db	9 NGLV-YLPFLLILAILFSTPVYWLVGLNPSFMAFLHFSLLIWLILYTANSVVVCFSALVP 527

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530 ----GOSVVSVATLLMTICFVFMMIFSGLLVNLTTIASWLSWLOYFSIPRYGFTALOHNE 585
Qу
                                               : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | | : : | : | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                  528 NFIVGNSVISG---VMGSFF----LFSGYFISNHEIPGYWIFMHYISLFKYPFEGFLINE 580
Πh
                 586 FLGONFCPGLNATGNNPCNYATCTGEEYLVKOGIDLSPWG---LWKNHVALACMIVIFLT 642
QУ
                                              1 1
                                                                      11 1:1:
                                                                                            : 1
                                                                                                       | | : | | : | ::::
                  581 FSKSNKC---LEYGFGKC----LVTEEDLLKE----ERYGEESRWRNVVIMLCFVLLYRF 629
Πh
                 643 IAYLKL 648
0v
                         1:1: 1
Dh
                 630 ISYVIL 635
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T47652
ABC transporter-like protein - Arabidopsis thaliana
N; Alternate names: protein T26I12.10
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C; Accession: T47652
R; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.;
Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, February 2000
A; Reference number: Z24471
A:Accession: T47652
A; Status: preliminary
A; Molecule type: DNA
A:Residues: 1-725 <MON>
A;Cross-references: UNIPROT: 09M3D6; UNIPARC: UPI00000A7A62; EMBL: AL132954
A; Experimental source: cultivar Columbia; BAC clone T26I12
C: Genetics:
A:Map position: 3
A; Note: T26I12.10
C; Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-
binding cassette homology
   Query Match
                                              22.2%; Score 745; DB 2; Length 725;
   Best Local Similarity 29.3%: Pred. No. 2.4e-44:
   Matches 193; Conservative 130; Mismatches 274; Indels 62; Gaps
                    36 VLSFHNICYRVKLKSGFLPCRKPVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLA 94
Qv
                          Db
                    72 VLNFNNLQYDVTLRRRFGFSRQNGVKTLLDDVSGEASDGDILAVLGASGAGKSTLIDALA 131
                    95 ARKDPSGLSGDVLINGAP--RPANFKCNSGYVVQDDVVMGTLTVRENLQFSAALRLATIM 152
                                     132 GRVAEGSLRGSVTLNGEKVLQSRLLKVISAYVMQDDLLFPMLTVKETLMFASEFRLPRSL 191
Dh
                 153 TNHEKNERINRVIQELGLDKVADSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLDEP 212
                         192 SKSKKMERVEALIDQLGLRNAANTVIGDEGHRGVSGGERRRVSIGIDIIHDPIVLFLDEP 251
Db
                 213 TTGLDSSTANAVLLLLKRMSKQGRTIIFSIHQPRYSIFKLFDSLTLLASGRLMFHGPAQE 272
                         Db
                  252 TSGLDSTNAFMVVQVLKRIAQSGSIVIMSIHQPSARIVELLDRLIILSRGKSVFNGSPAS 311
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273 ALGYFESAGYHCEAYNNPADFFLDII-----NGDSTAVALNREEDFKATEIIEPS--- 322
Qv
                      | ::| ||:: |
             1:1 1
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Db
        312 LPGFFSDFGRPIPEKENISEFALDLVRELEGSNEGTKALVDFNEKWOONKISLIOSAPOT 371
        323 ---KODKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKKITVFKEISYTTSFCHQLRW 379
               Db
        372 NKLDQDRSLSLKEA---INASV---SRGKL--VSGSSRSNPTSMETVSSYANPSLFETFI 423
        380 VSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFLTTNQCF 439
            Db
        424 LAKRYMKNWIRMPELVGTRIATVMVTGCLLATVYWKLDHTPRGAQERLTLFAFVVPTMFY 483
        440 SSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLPMTMLPSIIFTCIVYFMLGL 499
             Db
        484 CCLDNVPVFIQERYIFLRETTHNAYRTSSYVISHSLVS-LPQLLAPSLVFSAITFWTVGL 542
        500 KPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLLMTICFVFMMIFSGLLVNLT 559
                    : 1
        543 SGGLEGFVFYCLLIYASFWSGSSVVTFISGVVPNIMLCYMVSITYLAYCLLLSGFYVNRD 602
Db
        560 TIASWLSWLQYFSIPRYGFTALQHNEFLGQNFC------PGLNATG----- 599
Qv
            603 RIPFYWTWFHYISILKYPYEAVLINEFDDPSRCFVRGVQVFDSTLLGGVSDSGKVKLLET 662
        600 ----NNPCNYATC--TGEEYLVKQGI-DLSPWGLWKNHVALACMIVIFLTIAYLKLLF 650
                     Db
        663 LSKSLRTKITESTCLRTGSDLLAOOGITOLSKWD-----CLWITFASGLFFRILF 712
RESHLT 9
T45891
ABC transporter-like protein - Arabidopsis thaliana
N; Alternate names: protein F4P12.210
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45891
R; Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23016
A; Accession: T45891
A; Status: preliminary
A; Molecule type: DNA
A:Residues: 1-739 <BLO>
A; Cross-references: UNIPROT: Q9LFG8; UNIPARC: UPI000000A86EE; EMBL: AL132966
A: Experimental source: cultivar Columbia: BAC clone F4P12
C; Genetics:
A; Map position: 3
A; Note: F4P12.210
C; Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-
binding cassette homology
 Query Match
                      22.1%; Score 741.5; DB 2; Length 739;
 Best Local Similarity 28.3%; Pred. No. 4.4e-44;
 Matches 193; Conservative 123; Mismatches 256; Indels 111; Gaps 17;
         36 VLSFHNICYRVKLKSGF--LPC--RKPVE-----KEILSNINGIMKPG-LNAILGPT 82
Qv
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| | :|: |:| : | : |:|| :

1111 :: 1 11:1 1 11 1:

# RESULT 10 H96552

hypothetical protein F5D21.8 [imported] - Arabidopsis thaliana

C: Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004 C:Accession: H96552

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.

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Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.;
Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.;
Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti,
R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.;
Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.
J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.;
Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
A; Accession: H96552
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-678 <STO>
A; Cross-references: UNIPROT:Q9C8J8; UNIPARC:UPI00000A045D; GB:AE005173; NID:q10092361; PIDN:
AAG12770.1; GSPDB:GN00141
C; Genetics:
A;Gene: F5D21.8
A; Map position: 1
C; Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-
binding cassette homology
 Query Match
                       22.0%; Score 739; DB 2; Length 678;
 Best Local Similarity
                       30.3%; Pred. No. 5.8e-44;
 Matches 186; Conservative 137; Mismatches 248; Indels 42; Gaps
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Qy
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          28 KRLLNGVNGCGEPNRILAIMGPSGSGKSTLLDALAGRL--AGNVVMSGKVLVNGKKRRLD 85
Db
         117 FKCNSGYVVODDVVMGTLTVRENLOFSAALRLATTMTNHEKNERINRVIOELGLDKVADS 176
                : || |:||::||||||::::|
         86 FGA-AAYVTOEDVLLGTLTVRESISYSAHLRLPSKLTREEISDIVEATITDMGLEECSDR 144
Db
         177 KVGTOFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKOGR 236
                 145 TIGNWHLRGISGGEKKRLSIALEVLTKPSLLFLDEPTSGLDSASAFFVVOILRNIASSGK 204
         237 TIIFSIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLD 296
            Db
         205 TVVSSIHOPSGEVFALFDDLLLLSGGETVYFGEAESATKFFGEAGFPCPSRRNPSDHFLR 264
         297 IINGD----STAVALNR---EEDFKATEIIEPSKODKPLIEKLAEIYVNSSFYKETKAEL 349
              : | | : |: : | : | :: | : | | :: | |
         265 CVNSDFDNVTAALVESRRINDSSFSLHQLHETTNTLDPL-DDIPTAEIRTTLVRKFKCSL 323
         350 HOLSGGEKKKKITVF-----KEISYTTSFCHOLRWVSKRSFKNLLGNPOASIAOIIVTV 403
            : : :::
                              ::
                                     1:: [[] :::[[] ]: :
         324 YAAASRARIOEIASIVGIVTERKKGSOTNWWKOLRILTORSFINMSRDLGYYWMRIAVYI 383
Db
         404 VLGLVIGAIYFGLKNDSTGIONRAGVLFFLTTNOCFSSVSAVELFVVEKKLFIHEYISGY 463
            384 VLSICVGSIFFNVGRNHTNVMSTAACGGFMAGFMTFMSIGGFOSFIEEMKVFSRERLNGH 443
Dh
         464 YRVSSYFLGKLLSDLLPMTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSM 523
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1:
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Dh
        524 ALAIAAGOSVVSVATLLMTIC----FVFMMIFSGLLVNLTTIASWLSWLOYFSIPRYGFT 579
                   | || : :::::
                                                 : 1 | 11
        503 MMMIAS-----VVPNFLMGVMLGAGYIGIMVLSAGFFRFFPDLPMVFWRYPVSYINYGAW 557
Db
        580 ALO---HNEFLGONFCPGLNATGNNPCNYATCTGEEYLVKOGIDLSPWGLWKNHVALACM 636
           558 ALOGAYKNEMIGVEY-----DSPLPLVPKMKGELILOTVLGINPESSKWLDLAVVMM 609
        637 IVIFLTIAYLKLL 649
Qу
        610 ILIGYRIAFFAIL 622
Dh
RESULT 11
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ABC transporter-like protein - Arabidopsis thaliana
N; Alternate names: protein T15C9.110
C; Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 09-Jul-2004
C; Accession: T47650
R; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24470
A:Accession: T47650
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-708 < MEW>
A; Cross-references: UNIPROT: Q9M2V5; UNIPARC: UPI00000A627B; EMBL: AL132970
A; Experimental source: cultivar Columbia; BAC clone T15C9
C:Genetics:
A: Map position: 3
A:Note: T15C9.110
C; Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-
binding cassette homology
 Ouerv Match
                     21.7%: Score 726.5: DB 2: Length 708:
 Best Local Similarity 30.1%; Pred. No. 4.7e-43;
 Matches 198; Conservative 123; Mismatches 282; Indels 55; Gaps
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         36 VLSFHNICYRVKLKSGFLPCRKPVE--KEILSNINGIMKPG-LNAILGPTGGGKSSLLDV 92
           62 LLSFNNLSYNVVLRRRFDFSRRKTASVKTLLDDITGEARDGEILAVLGGSGAGKSTLIDA 121
Db
         93 LAARKDPSGLSGDVLINGAP--RPANFKCNSGYVVQDDVVMGTLTVRENLQFSAALRLAT 150
                   Db
        122 LAGRVAEDSLKGTVTLNGEKVLOSRLLKVISAYVMODDLLFPMLTVKETLMFASEFRLPR 181
        151 TMTNHEKNERINRVIOELGLDKVADSKVGTOFIRGVSGGERKRTSIGMELITDPSILFLD 210
0v
                Πh
        182 SLPKSKKMERVETLIDQLGLRNAADTVIGDEGHRGVSGGERRRVSIGIDIIHDPILLFLD 241
        211 EPTTGLDSSTANAVLLLLKRMSKOGRTIIFSIHOPRYSIFKLFDSLTLLASGRLMFHGPA 270
Οv
           Db
        242 EPTSGLDSTNAFMVVQVLKRIAQSGSVVIMSIHQPSARIIGLLDRLIILSHGKSVFNGSP 301
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271 OEALGYFESAGYHCEAYNNPADFFLDII----NGDSTAVALNREEDFKATEIIEPSKOD 325
Qу
                302 VSLPSFFSSFGRPIPEKENITEFALDVIRELEGSSEGTRDLVEFNEKWOONOTARATTOS 361
Πh
        326 KPLIEKLAEIYVNSSFYKETKAELHOLSGGEKKKKITVFKEISYTTSFCHOLRWVSKRSF 385
QУ
                   :: :| :|| |
                                                      362 RVSLKEAIAASV-----SRGKL--VSGSSGANPISMETVSSYANPPLAETFILAKRYI 412
Πh
        386 KNLLGNPOASIAOIIVTVVLGLVIGAIYFGLKNDSTGIONRAGVLFFLTTNOCFSSVSAV 445
            413 KNWIRTPELIGMRIGTVMVTGLLLATVYWRLDNTPRGAOERMGFFAFGMSTMFYCCADNI 472
Db
        446 ELEVVEKKLETHEYTSGYYRVSSYFLGKLLSDLLPMTMLPSTTETCTVYFMLGLKPKADA 505
             473 PVFIOERYIFLRETTHNAYRTSSYVISHALVS-LPOLLALSIAFAATTFWTVGLSGGLES 531
Db
        506 FFVMMFTLMMVAYSASSMALAIAAGOSVVSVATLLMTICFV-FMMIFSGLLVNLTTIASW 564
                Dh
        532 FFYYCLIIYAAFWSGSSIVTFI-SGLIPNVMMSYMVTIAYLSYCLLLGGFYINRDRIPLY 590
        565 LSWLOYFSIPRYGFTALOHNEFLGONFC------PGLNATG 599
Οv
             | | | : : | : | : | | | : |
        591 WIWFHYISLLKYPYEAVLINEFDDPSRCFVKGVOVFDGTLLAEVSHVMKVKLLDTLSGSL 650
Db
        600 NNPCNYATC--TGEEYLVKOGI-DLSPWG-LWKNHVALACMIVIFLTIAYLKLLFLKK 653
Οv
                 651 GTKITESTCLRTGPDLLMOOGITOLSKWDCLW---ITLAWGL-FFRILFYLSLLFGSK 704
RESULT 12
T08934
hypothetical protein F27G19.20 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C; Accession: T08934
R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.
submitted to the Protein Sequence Database, May 1999
A; Reference number: Z16519
A; Accession: T08934
A; Molecule type: DNA
A:Residues: 1-635 <BEV>
A; Cross-references: UNIPROT: Q9SZR9; UNIPARC: UPI000000A1E91; EMBL: AL078467; GSPDB: GN00062;
ATSP:F27G19.20
A; Experimental source: cultivar Columbia; BAC clone F27G19
C; Genetics:
A; Gene: ATSP:F27G19.20
A: Map position: 4
A; Introns: 38/3; 253/1; 304/1; 414/3
C: Superfamily: fruit fly white protein: ATP-binding cassette homology
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21.5%; Score 721; DB 2; Length 635;

1 MSSSNVEVFIPVSOGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSG---FLPCRK 57

http://es/ScoreAccessWeb/GetItem.action?AppId=099610...7\_142911\_us-09-961-086a-1.mpr&ItemType=4&startByte=0 (18 of 24)9/22/2008 12:04:28 PM

Matches 203; Conservative 121; Mismatches 284; Indels 68; Gaps

Best Local Similarity 30.0%; Pred. No. 9.7e-43;

Query Match

Οv

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            61 TEERTILKGLTGIVKPGEILAMLGPSGSGKTSLLTALGGRVGEGKGKLTGNISYNNKPLS 120
Db
       115 ANFKCNSGYVVODDVVMGTLTVRENLOFSAALRLATTMTNHEKNERINRVIOELGLDKVA 174
             Πh
       121 KAVKRTTGFVTODDALYPNLTVTETLVFTALLRLPNSFKKOEKIKOAKAVMTELGLDRCK 180
       175 DSKVGTOFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKO 234
Qу
          Dh
       181 DTIIGGPFLRGVSGGERKRVSIGOEILINPSLLFLDEPTSGLDSTTAORIVSILWELARG 240
       235 GRTIIFSIHOPRYSIFKLFDSLTLLASGRLMFHGPAOEALGYFESAGYHCEAYN-NPADF 293
                            : | :: | |: || |
       241 GRTVVTTIHOP-----SKGNPVYFGLGSNAMDYFASVGYSPLVERINPSDF 286
Dh
       294 FLDIINGDSTAVALNREEDFKATEIIEPSKODKPLIEKLAEIYVNSSFYK----E 344
           287 LLDIANGKPLLV-----ISCWPSVGSDESORPEAMKAALV---AFYKTNLLDSVINE 335
       345 TKAELHOLSGGEKKKKITVFKEISYTTSFCHOLRWVSKRSFKNLLGNPOA--SIAOIIVT 402
           336 VKGODDLCNKPRESSRVATNTYGDWPTTWWOOFCVLLKRGLKORRHDSFSGMKVAOIF-- 393
Dh
        403 VVLGLVIGAIYFGLKNDSTGIONRAGVLFFLTTNOCFSSV-SAVELFVVEKKLFIHEYIS 461
0v
           :: : | ::: | ::|::|:|||::: | : : | | :: | |
Dh
       394 -IVSFLCGLLWWOTK--ISRLODOIGLLFFISSFWAFFPLFOOIFTFPOERAMLOKERSS 450
       462 GYYRVSSYFLGKLISDLI.PMTMLPSTTFTCTVYFMLGLKPKADAFFVMMFTLMMVAYSAS 521
           451 GMYRLSPYFLSRVVGD-LPMELILPTCFLVITYWMAGLNHNLANFFVTLLVLLVHVLVSG 509
Db
       522 SMALAIAAGQSVVSVATLLMTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTAL 581
           510 GLGLALGALVMDOKSATTLGSVIMLTFLLAGGYYVOHVPV--FISWIKYVSIGYYTYKLL 567
       582 OHNEFLGONFCPGLNATGNN---PCNYATCTGEEYL-VKQGIDLSPWGLWKNHVALACMI 637
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       568 ----ILGQYTANELYPCGDNGKLRCHVGDFEGIKHIGFNSGL-----VSALALTAML 615
Dh
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       616 VVYRVIAYIALTRIGK 631
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## RESULT 13 G84791

probable ABC transporter [imported] - Arabidopsis thaliana

C; Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: G84791

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.;
Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanāken, S.E.;

```
Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.
M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.;
Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A; Accession: G84791
A; Status: preliminary
A; Molecule type: DNA
A:Residues: 1-755 <STO>
A; Cross-references: UNIPROT: Q9ZUTO; UNIPARC: UPI000000A1BA9; GB: AE002093; NID: q4056489; PIDN:
AAC98055.1; GSPDB:GN00139
C; Genetics:
A:Gene: At2q37360
A; Map position: 2
C; Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-
binding cassette homology
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           Db
         63 SSRALGIASPINSA-ASSFNSWASAPASSISSSPFVLSFTDLTYSVKIQKKFNPLACCRR 121
Qv
         58 PVE-----KEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLING 110
                   122 SGNDSSVNTKILLNGISGEAREGEMMAVLGASGSGKSTLIDALANRIAKDSLRGSITLNG 181
        111 APRPANF-KCNSGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELG 169
               Db
        182 EVLESSMOKVISAYVMODDLLFPMLTVEETLMFSAEFRLPRSLSKKKKKARVOALIDOLG 241
        170 LDKVADSKVGTOFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLK 229
Qv
           Πh
        242 LRSAAKTVIGDEGHRGVSGGERRRVSIGNDIIHDPIILFLDEPTSGLDSTSAYMVIKVLO 301
        230 RMSKOGRTIIFSIHOPRYSIFKLFDSLTLLASGRLMFHGPAOEALGYFESAGYHCEAYNN 289
           302 RIAQSGSIVIMSIHQPSYRIMGLLDQLIFLSKGNTVYSGSPTHLPQFFSEFKHPIPENEN 361
Db
        290 PADFFLDIINGDSTAVALNREEDFKATEIIEPSKODKPLIE-----KLAEIYVN---- 338
             362 KTEFALDLI-----RELEYS-----TEGTKPLVEFHKOWRAKOAPSYNNNKR 404
Db
        339 ----SSFYKETKAELHQ---LSGGEKKKKITVFKEI-SYTTSFCHQLRWVSKRSFKNLLG 390
               Db
        405 NTNVSSLKEAITASISRGKLVSGATNNNSSNLTPSFOTFANPFWIEMIVIGKRAILNSRR 464
        391 NPOASIAOIIVTVVLGLVIGAIYFGLKNDSTGIONRAGVLFFLTTNOCFSSVSAVELFVV 450
0v
                Πh
        465 QPELLGMRLGAVMVTGIILATMFTNLDNSPKGAQERLGFFAFAMSTTFYTCAEAIPVFLQ 524
        451 EKKLFIHEYISGYYRVSSYFLGKLLSDLLPMTMLPSIIFTCIVYFMLGLKPKADAFFVMM 510
                    525 ERYIFMRETAYNAYRRSSYVLSOSIIS-IPALIVLSASFAATTFWAVGLDGGANGFFFFY 583
Db
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Qу

Πh

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571 FSIPRYGFTALQHNEFLGQN----FCPGLNATGNNP-----C 603
QУ
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         644 ISLVKYPYEGVLONEF--ONPTRCFARGVOLFDNSPLGEFPNDVKVNLLKSMSGVLGTNV 701
         604 NYATC--TGEEYLVKOGI-DLSPWG-LWKNHVALACMIVIFLTIA---YLKLLF 650
                Dh
         702 TAETCVTTGIDILKOOGITDISKWNCLW-----ITVAWGFFFRVLF 742
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T02567
probable ATP-binding cassette protein T16B24.1 - Arabidopsis thaliana
N; Alternate names: protein F12L6.1
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: T02567; T00545; C84816
R; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.
M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
submitted to the EMBL Data Library, August 1998
A; Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A; Reference number: Z14679
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A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-740 < ROU>
A; Cross-references: UNIPROT:080946; UNIPARC:UPI000000AC233; EMBL:AC004697; NID:q3402671;
PIDN: AAC28975.1; PID: q3402672
A; Experimental source: cultivar Columbia
R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
S.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
submitted to the EMBL Data Library, July 1998
A; Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.
A; Reference number: Z14168
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A; Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-362 < ROW>
A:Cross-references: UNIPARC:UPI00001746D9: EMBL:AC004218: NID:g3355463: PIDN:AAC27826.1:
PID:q3355464
A: Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.;
Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.;
Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.
M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.;
Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A:Accession: C84816
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511 FTLMMVAYSASSMALAIAAGOSVVSVATLLMTICFVFMMIFSGLLVNLTTIASWLSWLOY 570

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A; Status: preliminary A; Molecule type: DNA

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A; Gene: At2q39350; T16B24.1; F12L6.1
A; Map position: 2
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binding cassette homology
C; Keywords: ATP
F:110-310/Domain: ATP-binding cassette homology <ABC>
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Db
        70 IMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPAN-FKCNSGYVVOD 127
             116 ETRDGEIMAVLGASGSGKSTLIDALANRIAKGSLKGTVKLNGETLOSRMLKVISAYVMOD 175
Db
       128 DVVMGTLTVRENLOFSAALRLATTMTNHEKNERINRVIOELGLDKVADSKVGTOFIRGVS 187
Οv
           176 DLLFPMLTVEETLMFAAEFRLPRSLPKSKKKLRVOALIDOLGIRNAAKTIIGDEGHRGIS 235
Dh
       188 GGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKOGRTIIFSIHOPRY 247
0v
           Dh
       236 GGERRRVSIGIDIIHDPILLFLDEPTSGLDSTSAFMVVKVLKRIAQSGSIVIMSIHOPSH 295
       248 SIFKLFDSLTLLASGRLMFHGPAOEALGYFESAGYHCEAYNNPADFFLDII-----NG 300
Οv
            296 RVLGLLDRLIFLSRGHTVYSGSPASLPRFFTEFGSPIPENENRTEFALDLIRELEGSAGG 355
Db
       301 DSTAVALNREEDFKATEIIEPSKODKPLIEKLAEIYVNSSFYKETKAELHO---LSGGEK 357
0v
              : |: | |::|:|| : ||:: |:: :|||
        356 TRGLIEFNK----KWOEMKKOSNROPPLTPP-SSPYPNLTLKEAIAASISRGKLVSGGES 410
       358 -----KKKITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGA 411
                  411 VAHGGATINTTTLAVPAFANPMWIEIKTLSKRSMLNSRROPELFGIRIASVVITGFILAT 470
Dh
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           471 VFWRLDNSPKGVQERLGFFAFAMSTMFYTCADALPVFLQERYIFMRETAYNAYRRSSYVL 530
Db
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       531 SHAIVS-FPSLIFLSVAFAATTYWAVGLDGGLTGLLFYCLIILASFWSGSSFVTFLSGVV 589
       532 SVVSVATLLMTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNF 591
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       590 PSVMLGYTIVVAILAYFLLFSGFFINRNRIPDYWIWFHYMSLVKYPYEAVLQNEFSDATK 649
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Db

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650 CFVRGVQIFDNTPLGELPEVMKLKLLGTVSKSLGVTISSTTCLTTGSDILRQQGVVQLSK 709
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RESHLT 15
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: E96742
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.;
Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.;
Creasy, T.H.; Dewar, K.; Dunn, P.; Etqu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.;
Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.;
Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti,
R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.;
Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.
J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.;
Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
A; Accession: E96742
A; Status: preliminary
A; Molecule type: DNA
A:Residues: 1-609 <STO>
A; Cross-references: UNIPROT: 09C8W6; UNIPARC: UPI000009EF81; GB: AE005173; NID: q6978921; PIDN:
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C; Genetics:
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A; Map position: 1
C; Superfamily: fruit fly white protein; ATP-binding cassette homology
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             143 NTVVGNTFIRGISGGERKRVSIAHELLINPSLLVLDEPTSGLDATAALRLVOTLAGLAHG 202
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Qy

Db

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